



SEQUENCE LISTING

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TECH CENTER 1600/2900

<110> Hill, Ronald J.
Hannan, Garry N.

<120> Genetic Sequences Encoding Steroid and Juvenile Hormone
Receptor Polypeptides and Insecticidal Modalities
Therefor

<130> 53-99

<140> 09/346,470

<141> 1999-07-01

<150> WO 99/00033

<151> 1999-01-15

<150> AU PP1356/98

<151> 1998-01-15

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<170> PatentIn Ver. 2.0

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<212> DNA

<213> Lucilia cuprina

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<221> CDS

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His His Met Asn Asn Ser Ser Met Met His His Thr Pro Arg Ser Glu	
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Cys Gly Asp Pro Met Ser Leu Val Phe Phe Ala Lys Leu Leu Ser Ile	
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 65 70 75 80

Ser Ser Leu Pro Ala Gln Thr Thr Ile Ile Pro Leu Ser Ala Leu Pro
 85 90 95

Asn Ser Asn Asn Ala Ser Leu Asn Asn Gln Asn Gln Asn Tyr Gln Asn
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195	200	205	
Leu Asn Ser Leu Gln Ala Ser Gln Asn Gly Gln Val Ile His Ala Asn			
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Leu Lys Arg Ile Met Ser Ser Pro Asp Glu Asn Glu Ser Gln His Asp	465	470	475
Ala Ser Phe Arg His Ile Thr Glu Ile Thr Ile Leu Thr Val Gln Leu	485	490	495
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Gln Ser Tyr Tyr Ile Asp Thr Leu Arg Ile Tyr Ile Leu Asn Arg His	610	615	620
Cys Gly Asp Pro Met Ser Leu Val Phe Phe Ala Lys Leu Leu Ser Ile	625	630	635
Leu Thr Glu Leu Arg Thr Leu Gly Asn Gln Asn Ala Glu Met Cys Phe	645	650	655
Ser Leu Lys Leu Lys Asn Arg Lys Leu Pro Lys Phe Leu Glu Glu Ile	660	665	670

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 Ser Ser Tyr Ser Pro Lys Pro Gly Ser Pro Asn Pro Phe Ala Ile Gly
 35 40 45
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 Leu Gln Ala Ile Asn Ala Val Ala Ala Ala Asn Ala Asn Asn Gln Asn
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Ala Ser Gly Lys His Tyr Gly Val Tyr Ser Cys Glu Gly Cys Lys Gly	
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ttc ttc aaa cgt acc gta cgc aag gac ttg aca tat gct tgt cgt gag	384
Phe Phe Lys Arg Thr Val Arg Lys Asp Leu Thr Tyr Ala Cys Arg Glu	
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Cys Arg Tyr Gln Lys Cys Leu Ala Cys Gly Met Lys Arg Glu Ala Val	
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 50 55 60
 Gln Met Leu Gln Thr Thr Pro Pro Gln Gln Gln Gln Tyr Pro Pro Asn
 65 70 75 80
 His Pro Leu Ser Gly Ser Lys His Leu Cys Ser Ile Cys Gly Asp Arg
 85 90 95
 Ala Ser Gly Lys His Tyr Gly Val Tyr Ser Cys Glu Gly Cys Lys Gly
 100 105 110
 Phe Phe Lys Arg Thr Val Arg Lys Asp Leu Thr Tyr Ala Cys Arg Glu
 115 120 125
 Asp Arg Asn Cys Ile Ile Asp Lys Arg Gln Arg Asn Arg Cys Gln Tyr
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 Cys Arg Tyr Gln Lys Cys Leu Ala Cys Gly Met Lys Arg Glu Ala Val
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 Gln Glu Glu Arg Gln Arg Gly Thr Arg Ala Ala Asn Ala Arg Ala Ala
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 Gly Ala Gly Gly Gly Gly Gly Gly Gly Gly Gly Val Ser Asn Val Val
 180 185 190
 Gly Ala Gly Gly Glu Asp Phe Lys Pro Ser Ser Ser Leu Arg Asp Leu
 195 200 205
 Thr Ile Glu Arg Ile Ile Glu Ala Glu Gln Lys Ala Glu Ser Leu Ser
 210 215 220
 Gly Asp Asn Val Leu Pro Phe Leu Arg Val Gly Asn Asn Ser Met Val
 225 230 235 240

Gln His Asp Tyr Lys Gly Ala Val Ser His Leu Cys Gln Met Val Asn
 245 250 255

Lys Gln Leu Tyr Gln Met Val Glu Tyr Ala Arg Arg Thr Pro His Phe
 260 265 270

Thr His Leu Gln Arg Glu Asp Gln Ile Leu Leu Leu Lys Ala Gly Trp
 275 280 285

Asn Glu Leu Leu Ile Ala Asn Val Ala Trp Cys Ser Ile Glu Ser Leu
 290 295 300

Asp Ala Glu Tyr Ala Ser Pro Gly Thr Val His Asp Gly Ser Phe Gly
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Arg Arg Ser Pro Val Arg Gln Pro Gln Gln Leu Phe Leu Asn Gln Asn
 325 330 335

Phe Ser Tyr His Arg Asn Ser Ala Ile Lys Ala Asn Val Val Ser Ile
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Phe Asp Arg Ile Leu Ser Glu Leu Ser Ile Lys Met Lys Arg Leu Asn
 355 360 365

Ile Asp Arg Ser Glu Leu Ser Cys Leu Lys Ala Ile Ile Leu Phe Asn
 370 375 380

Pro Asp Ile Arg Gly Leu Lys Cys Arg Ala Asp Val Glu Val Cys Arg
 385 390 395 400

Glu Lys Ile Tyr Ala Cys Leu Asp Glu His Cys Arg Thr Glu His Pro
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Gly Asp Asp Gly Arg Phe Ala Gln Leu Leu Arg Leu Pro Ala Leu
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Arg Ser Ile Ser Leu Lys Cys Leu Asp His Leu Phe Phe Phe Arg Leu
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Pro Ile Cys
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Leu Ile Leu Ile Phe Leu Leu Leu Phe Leu Trp Arg Leu Leu Ala Phe	
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Arg Phe Leu Phe Ile Ser Glu Gln Pro Pro Pro Glu Glu Leu Cys Leu	
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115 120 125	
gag aaa aaa gct caa cga gaa aaa gat aaa cca aat tct act aca gac	432
Glu Lys Lys Ala Gln Arg Glu Lys Asp Lys Pro Asn Ser Thr Thr Asp	
130 135 140	
att tct cct gaa ata ata aaa ata gaa cct aca gag atg aag att gaa	480
Ile Ser Pro Glu Ile Ile Lys Ile Glu Pro Thr Glu Met Lys Ile Glu	
145 150 155 160	
tgt ggt gaa cca atg ata atg ggc aca cct atg ccg act gta cct tac	528
Cys Gly Glu Pro Met Ile Met Gly Thr Pro Met Pro Thr Val Pro Tyr	
165 170 175	

gtg aaa cct ttg agt tct ctc gtg ccg aat tcg gca cga gtc acg ggt 576
 Val Lys Pro Leu Ser Ser Leu Val Pro Asn Ser Ala Arg Val Thr Gly
 180 185 190

tac aaa ttt 585
 Tyr Lys Phe
 195

<210> 6
 <211> 195
 <212> PRT
 <213> Myzus persicae

<400> 6
 Glu Phe Gly Thr Ser Ala Ile Val Asn Gly Phe Ile Arg Thr Ile Ser
 1 5 10 15

Leu Ile Leu Ile Phe Leu Leu Leu Phe Leu Trp Arg Leu Leu Ala Phe
 20 25 30

Arg Phe Leu Phe Ile Ser Glu Gln Pro Pro Pro Glu Glu Leu Cys Leu
 35 40 45

Val Cys Gly Asp Arg Ser Ser Gly Tyr His Tyr Asn Ala Leu Thr Cys
 50 55 60

Glu Gly Cys Lys Gly Phe Phe Arg Arg Ser Ile Thr Lys Asn Ala Val
 65 70 75 80

Tyr Gln Cys Lys Tyr Gly Asn Asn Cys Glu Ile Asp Met Tyr Met Arg
 85 90 95

Arg Lys Cys Gln Glu Cys Arg Leu Lys Lys Cys Leu Thr Val Gly Met
 100 105 110

Arg Pro Glu Cys Val Val Pro Glu Val Gln Cys Ala Val Lys Arg Lys
 115 120 125

Glu Lys Lys Ala Gln Arg Glu Lys Asp Lys Pro Asn Ser Thr Thr Asp
 130 135 140

Ile Ser Pro Glu Ile Ile Lys Ile Glu Pro Thr Glu Met Lys Ile Glu
 145 150 155 160

Cys Gly Glu Pro Met Ile Met Gly Thr Pro Met Pro Thr Val Pro Tyr
 165 170 175

Val Lys Pro Leu Ser Ser Leu Val Pro Asn Ser Ala Arg Val Thr Gly
 180 185 190

Tyr Lys Phe
195

<210> 7
<211> 208
<212> DNA
<213> Myzus persicae

<400> 7
catgcctgca ggtcgactct agaggatccc ctcgctcggg taccattaca acgcactcac 60
ctgtgaaggc tgtaaggggt tctttcgacg gagtggtacc aaaaatgcgg tgtattgttg 120
taaatttggg catgcctgcg aaatggacat gtatatgca cgtaaagtgc aggaatgtag 180
gctgaaaaaa tgtttggtg tgggcatg 208

<210> 8
<211> 436
<212> DNA
<213> Myzus persicae

<400> 8
catgcggccg gaatgtgtgg tgcccga aaa ccagtgtgca atgaaacgac gcgaaaagaa 60
agcacaaaaa gagaaggata aaatacagac cagtgtgtgt gcaacggaaa ttaaaaagga 120
aatactcgat ttaatgacat gtgaaccgcc atcacatcca acgtgtccgc tgttacctga 180
agacattttg gctaaatgtc aagctcgtaa tatacctcct ttatcgta atcaattggc 240
agttatatat aaattaatat ggtatcaaga tggctacgaa cagccatccg aggaagatct 300
caaacgtata atgagttcac ccgatgaaa tgaaagtcaa cacgatgcat catttcgtca 360
tataacagaa atcactatac taacagtaca attaattggt gaatgtgcca aaggtctagg 420
gtaccgagct cgaatt 436

<210> 9
<211> 1797
<212> DNA
<213> Myzus persicae

<220>
<221> CDS
<222> (1) .. (1797)

<400> 9

atg atg gac cag aaa tgt gac gtc ggc ggt ggt ggt gtc gct gct gcc	48
Met Met Asp Gln Lys Cys Asp Val Gly Gly Gly Gly Val Ala Ala Ala	
1 5 10 15	
gcc gcc ggt atc ggt ggc ggc ggt gtc ggc ggc ctc atg tcg tac aac	96
Ala Ala Gly Ile Gly Gly Gly Gly Val Gly Gly Leu Met Ser Tyr Asn	
20 25 30	
cgt ggc cgt ggc ggc acc gag gtc atc atc aaa ccc cgt agt cct gcc	144
Arg Gly Arg Gly Gly Thr Glu Val Ile Ile Lys Pro Arg Ser Pro Ala	
35 40 45	
gtg gtg cag gtg gcc acc ggt ggc agt tac cac ggc ctg ccg gcg gcc	192
Val Val Gln Val Ala Thr Gly Gly Ser Tyr His Gly Leu Pro Ala Ala	
50 55 60	
tcc gac gcc gtc atc gtg cgc agc ccg cca ggc ggc cac ttg ccc ggg	240
Ser Asp Ala Val Ile Val Arg Ser Pro Pro Gly Gly His Leu Pro Gly	
65 70 75 80	
ccg cag cag caa gtg ccg ccg tcc cgc aac ggc tgt tcc acc ctg ttt	288
Pro Gln Gln Gln Val Pro Pro Ser Arg Asn Gly Cys Ser Thr Leu Phe	
85 90 95	
agc gac atc gct ggc gtc aag cga ctc agg ccc gac gat tgg ttg gcc	336
Ser Asp Ile Ala Gly Val Lys Arg Leu Arg Pro Asp Asp Trp Leu Ala	
100 105 110	
gtc aac tcg ccg ccc gcc tct tcg ccc ggc acg tcg cac ata tcc tac	384
Val Asn Ser Pro Pro Ala Ser Ser Pro Gly Thr Ser His Ile Ser Tyr	
115 120 125	
aca gtc ata tcg aac ggc ggc ggc ggt ggc ggc ggt ggc ggc ggt ggt	432
Thr Val Ile Ser Asn Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly	
130 135 140	
tac aac acg tct cca atg tcg acc aac agc tac gac ccg tac agt ccg	480
Tyr Asn Thr Ser Pro Met Ser Thr Asn Ser Tyr Asp Pro Tyr Ser Pro	
145 150 155 160	
atg agt gga aaa atc gtc aaa gaa gag ttg tct ccg cca aac agc ctg	528
Met Ser Gly Lys Ile Val Lys Glu Glu Leu Ser Pro Pro Asn Ser Leu	
165 170 175	
tcg gga gtc agc agc cat tcg gat ggg ttg aag aag aag aaa ctc aac	576
Ser Gly Val Ser Ser His Ser Asp Gly Leu Lys Lys Lys Lys Leu Asn	
180 185 190	

cac acg ccc tcg acc ggt gtc gtc aac acc tcg gca tcg ggc ccc ggg	624
His Thr Pro Ser Thr Gly Val Val Asn Thr Ser Ala Ser Gly Pro Gly	
195 200 205	
ggg ggc gtt ggt ggc aat gtg ctg aac aac cga cct ccc gaa gag ctg	672
Gly Gly Val Gly Gly Asn Val Leu Asn Asn Arg Pro Pro Glu Glu Leu	
210 215 220	
tgc ctg gtg tgt ggc gac cgg tcg tcc ggt tac cat tac aac gct ctc	720
Cys Leu Val Cys Gly Asp Arg Ser Ser Gly Tyr His Tyr Asn Ala Leu	
225 230 235 240	
aca tgc gaa gga tgc aag ggg ttc ttc cgg agg agc atc acc aag aac	768
Thr Cys Glu Gly Cys Lys Gly Phe Phe Arg Arg Ser Ile Thr Lys Asn	
245 250 255	
gcc gtg tac cag tgc aag tac ggc aac aat tgc gaa atc gac atg tac	816
Ala Val Tyr Gln Cys Lys Tyr Gly Asn Asn Cys Glu Ile Asp Met Tyr	
260 265 270	
atg agg cgg aag tgc cag gag tgc cgg ctg aaa aaa tgc ctg acc gtc	864
Met Arg Arg Lys Cys Gln Glu Cys Arg Leu Lys Lys Cys Leu Thr Val	
275 280 285	
ggc atg agg cct gaa tgt gtt gta cct gaa gtt caa tgc gca gta aaa	912
Gly Met Arg Pro Glu Cys Val Val Pro Glu Val Gln Cys Ala Val Lys	
290 295 300	
aga aag gag aaa aaa gct caa cga gaa aaa gat aaa cca aat tct act	960
Arg Lys Glu Lys Lys Ala Gln Arg Glu Lys Asp Lys Pro Asn Ser Thr	
305 310 315 320	
aca gac att tct cct gaa ata ata aaa ata gaa cct aca gag atg aag	1008
Thr Asp Ile Ser Pro Glu Ile Ile Lys Ile Glu Pro Thr Glu Met Lys	
325 330 335	
att gaa tgt ggt gaa cca atg ata atg ggc aca cct atg ccg act gta	1056
Ile Glu Cys Gly Glu Pro Met Ile Met Gly Thr Pro Met Pro Thr Val	
340 345 350	
cct tac gtg aaa cct ttg agt tct gaa caa aaa gaa ctg atc cac cga	1104
Pro Tyr Val Lys Pro Leu Ser Ser Glu Gln Lys Glu Leu Ile His Arg	
355 360 365	
ctt gtc tat ttc cag gat caa tat gaa gct cct agt gaa aaa gac atg	1152
Leu Val Tyr Phe Gln Asp Gln Tyr Glu Ala Pro Ser Glu Lys Asp Met	
370 375 380	
aaa cgt tta aca ata aat aat caa aat atg gat gaa tat gat gaa gaa	1200
Lys Arg Leu Thr Ile Asn Asn Gln Asn Met Asp Glu Tyr Asp Glu Glu	
385 390 395 400	

aaa caa agt gac acc aca tat cga atc atc act gag atg aca ata ctc	1248
Lys Gln Ser Asp Thr Thr Tyr Arg Ile Ile Thr Glu Met Thr Ile Leu	
405 410 415	
aca gtt caa ctg att gtt gag ttt gcc aaa cga tta cca ggt ttc gat	1296
Thr Val Gln Leu Ile Val Glu Phe Ala Lys Arg Leu Pro Gly Phe Asp	
420 425 430	
aaa ctt gta aga gaa gat caa atc act tta ctc aag gct tgc tca agt	1344
Lys Leu Val Arg Glu Asp Gln Ile Thr Leu Leu Lys Ala Cys Ser Ser	
435 440 445	
gaa gct atg atg ttc agg gta gca agg aag tat gac atc acc act gac	1392
Glu Ala Met Met Phe Arg Val Ala Arg Lys Tyr Asp Ile Thr Thr Asp	
450 455 460	
tca ata gtg ttt gct aac aac cag cca ttt tca gct gat tca tat aac	1440
Ser Ile Val Phe Ala Asn Asn Gln Pro Phe Ser Ala Asp Ser Tyr Asn	
465 470 475 480	
aaa gct gga ttg gga gat gcc att gaa aac caa ctg tca ttc agt cgg	1488
Lys Ala Gly Leu Gly Asp Ala Ile Glu Asn Gln Leu Ser Phe Ser Arg	
485 490 495	
ttt atg tac aat atg aag gtg gat aac gca gaa tat gcc tta ttg acc	1536
Phe Met Tyr Asn Met Lys Val Asp Asn Ala Glu Tyr Ala Leu Leu Thr	
500 505 510	
gcc atc gtc ata ttt tcg agt agg cca aat tta cta gat ggt tgg aaa	1584
Ala Ile Val Ile Phe Ser Ser Arg Pro Asn Leu Leu Asp Gly Trp Lys	
515 520 525	
gtg gag aaa atc caa gaa atc tac cta gag tcc tta aaa gct tat gta	1632
Val Glu Lys Ile Gln Glu Ile Tyr Leu Glu Ser Leu Lys Ala Tyr Val	
530 535 540	
gat aat cga gac cgt gac aca gca act gta cga tat gcg cga ctt ctc	1680
Asp Asn Arg Asp Arg Asp Thr Ala Thr Val Arg Tyr Ala Arg Leu Leu	
545 550 555 560	
tca gta ctt aca gaa ttg cgc aca tta ggc aat gaa aac tct gag cta	1728
Ser Val Leu Thr Glu Leu Arg Thr Leu Gly Asn Glu Asn Ser Glu Leu	
565 570 575	
tgt atg aca ctg aaa ctg aaa aac aga gta gta ccc cca ttc ttg gcc	1776
Cys Met Thr Leu Lys Leu Lys Asn Arg Val Val Pro Pro Phe Leu Ala	
580 585 590	
gaa ata tgg gat gtc atg cca	1797
Glu Ile Trp Asp Val Met Pro	
595	

<210> 10
 <211> 599
 <212> PRT
 <213> Myzus persicae

<400> 10

Met Met Asp Gln Lys Cys Asp Val Gly Gly Gly Gly Val Ala Ala Ala
 1 5 10 15

Ala Ala Gly Ile Gly Gly Gly Gly Val Gly Gly Leu Met Ser Tyr Asn
 20 25 30

Arg Gly Arg Gly Gly Thr Glu Val Ile Ile Lys Pro Arg Ser Pro Ala
 35 40 45

Val Val Gln Val Ala Thr Gly Gly Ser Tyr His Gly Leu Pro Ala Ala
 50 55 60

Ser Asp Ala Val Ile Val Arg Ser Pro Pro Gly Gly His Leu Pro Gly
 65 70 75 80

Pro Gln Gln Gln Val Pro Pro Ser Arg Asn Gly Cys Ser Thr Leu Phe
 85 90 95

Ser Asp Ile Ala Gly Val Lys Arg Leu Arg Pro Asp Asp Trp Leu Ala
 100 105 110

Val Asn Ser Pro Pro Ala Ser Ser Pro Gly Thr Ser His Ile Ser Tyr
 115 120 125

Thr Val Ile Ser Asn Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
 130 135 140

Tyr Asn Thr Ser Pro Met Ser Thr Asn Ser Tyr Asp Pro Tyr Ser Pro
 145 150 155 160

Met Ser Gly Lys Ile Val Lys Glu Glu Leu Ser Pro Pro Asn Ser Leu
 165 170 175

Ser Gly Val Ser Ser His Ser Asp Gly Leu Lys Lys Lys Lys Leu Asn
 180 185 190

His Thr Pro Ser Thr Gly Val Val Asn Thr Ser Ala Ser Gly Pro Gly
 195 200 205

Gly Gly Val Gly Gly Asn Val Leu Asn Asn Arg Pro Pro Glu Glu Leu
 210 215 220

Cys Leu Val Cys Gly Asp Arg Ser Ser Gly Tyr His Tyr Asn Ala Leu
 225 230 235 240

Thr	Cys	Glu	Gly	Cys	Lys	Gly	Phe	Phe	Arg	Arg	Ser	Ile	Thr	Lys	Asn	
				245					250					255		
Ala	Val	Tyr	Gln	Cys	Lys	Tyr	Gly	Asn	Asn	Cys	Glu	Ile	Asp	Met	Tyr	
			260					265					270			
Met	Arg	Arg	Lys	Cys	Gln	Glu	Cys	Arg	Leu	Lys	Lys	Cys	Leu	Thr	Val	
			275				280					285				
Gly	Met	Arg	Pro	Glu	Cys	Val	Val	Pro	Glu	Val	Gln	Cys	Ala	Val	Lys	
			290			295					300					
Arg	Lys	Glu	Lys	Lys	Ala	Gln	Arg	Glu	Lys	Asp	Lys	Pro	Asn	Ser	Thr	
305					310					315					320	
Thr	Asp	Ile	Ser	Pro	Glu	Ile	Ile	Lys	Ile	Glu	Pro	Thr	Glu	Met	Lys	
				325					330					335		
Ile	Glu	Cys	Gly	Glu	Pro	Met	Ile	Met	Gly	Thr	Pro	Met	Pro	Thr	Val	
			340					345					350			
Pro	Tyr	Val	Lys	Pro	Leu	Ser	Ser	Glu	Gln	Lys	Glu	Leu	Ile	His	Arg	
			355				360					365				
Leu	Val	Tyr	Phe	Gln	Asp	Gln	Tyr	Glu	Ala	Pro	Ser	Glu	Lys	Asp	Met	
			370			375					380					
Lys	Arg	Leu	Thr	Ile	Asn	Asn	Gln	Asn	Met	Asp	Glu	Tyr	Asp	Glu	Glu	
385					390					395					400	
Lys	Gln	Ser	Asp	Thr	Thr	Tyr	Arg	Ile	Ile	Thr	Glu	Met	Thr	Ile	Leu	
				405					410					415		
Thr	Val	Gln	Leu	Ile	Val	Glu	Phe	Ala	Lys	Arg	Leu	Pro	Gly	Phe	Asp	
			420					425					430			
Lys	Leu	Val	Arg	Glu	Asp	Gln	Ile	Thr	Leu	Leu	Lys	Ala	Cys	Ser	Ser	
			435				440					445				
Glu	Ala	Met	Met	Phe	Arg	Val	Ala	Arg	Lys	Tyr	Asp	Ile	Thr	Thr	Asp	
			450			455					460					
Ser	Ile	Val	Phe	Ala	Asn	Asn	Gln	Pro	Phe	Ser	Ala	Asp	Ser	Tyr	Asn	
465					470					475					480	
Lys	Ala	Gly	Leu	Gly	Asp	Ala	Ile	Glu	Asn	Gln	Leu	Ser	Phe	Ser	Arg	
				485					490					495		
Phe	Met	Tyr	Asn	Met	Lys	Val	Asp	Asn	Ala	Glu	Tyr	Ala	Leu	Leu	Thr	
			500					505					510			

Ala Ile Val Ile Phe Ser Ser Arg Pro Asn Leu Leu Asp Gly Trp Lys
515 520 525

Val Glu Lys Ile Gln Glu Ile Tyr Leu Glu Ser Leu Lys Ala Tyr Val
530 535 540

Asp Asn Arg Asp Arg Asp Thr Ala Thr Val Arg Tyr Ala Arg Leu Leu
545 550 555 560

Ser Val Leu Thr Glu Leu Arg Thr Leu Gly Asn Glu Asn Ser Glu Leu
565 570 575

Cys Met Thr Leu Lys Leu Lys Asn Arg Val Val Pro Pro Phe Leu Ala
580 585 590

Glu Ile Trp Asp Val Met Pro
595

<210> 11
<211> 1131
<212> DNA
<213> Myzus persicae

<220>
<221> CDS
<222> (1)..(1131)

<400> 11
atg tat tcc aac tcg tac acc atg tat tca agt gac aga tta tac agc 48
Met Tyr Ser Asn Ser Tyr Thr Met Tyr Ser Ser Asp Arg Leu Tyr Ser
1 5 10 15

gtc gat cgg aac agt atg atg aat aat tct tgc aac gta caa gac tct 96
Val Asp Arg Asn Ser Met Met Asn Asn Ser Cys Asn Val Gln Asp Ser
20 25 30

cgc aat tac ccg ccc aac cat cca ctc agc ggt tcg aaa cat ctg tgc 144
Pro Asn Tyr Pro Pro Asn His Pro Leu Ser Gly Ser Lys His Leu Cys
35 40 45

tcc ata tgc ggc gat cgc gcc agt gga aaa cat tac gga gtc tac agc 192
Ser Ile Cys Gly Asp Arg Ala Ser Gly Lys His Tyr Gly Val Tyr Ser
50 55 60

tgc gag ggg tgc aaa ggg ttc ttc aaa cgc aca gtg agg aaa aat ttg 240
Cys Glu Gly Cys Lys Gly Phe Phe Lys Arg Thr Val Arg Lys Asn Leu
65 70 75 80

tca tac gcg tgt cgc gaa gaa aac aaa tgc atc atc gac aag cgc caa 288
Ser Tyr Ala Cys Arg Glu Glu Asn Lys Cys Ile Ile Asp Lys Arg Gln

cga aat cgg tgc caa tac tgc agg tat caa aaa tgt ttg acc atg ggc	336
Arg Asn Arg Cys Gln Tyr Cys Arg Tyr Gln Lys Cys Leu Thr Met Gly	
100 105 110	
atg aaa aga gaa gct gtg cag gaa gaa aga caa cgt aca aaa gaa cga	384
Met Lys Arg Glu Ala Val Gln Glu Glu Arg Gln Arg Thr Lys Glu Arg	
115 120 125	
gat cat aat aac atc gaa gtt gaa ccc acg agc agt tct aat act gat	432
Asp His Asn Asn Ile Glu Val Glu Pro Thr Ser Ser Ser Asn Thr Asp	
130 135 140	
atg cca gtg gaa ctc ata tta agg gct gag aat aaa gct gat gct ata	480
Met Pro Val Glu Leu Ile Leu Arg Ala Glu Asn Lys Ala Asp Ala Ile	
145 150 155 160	
aag act gaa caa cag tat ata gag caa cga cat cct caa cat act gtt	528
Lys Thr Glu Gln Gln Tyr Ile Glu Gln Arg His Pro Gln His Thr Val	
165 170 175	
ggt gct att tgt caa gca act gac aag cag tta ata caa ctt gtt gaa	576
Gly Ala Ile Cys Gln Ala Thr Asp Lys Gln Leu Ile Gln Leu Val Glu	
180 185 190	
tgg gcc aag cat ata ccg cat ttt aaa aat tta cct cta ggc gat caa	624
Trp Ala Lys His Ile Pro His Phe Lys Asn Leu Pro Leu Gly Asp Gln	
195 200 205	
gtt tta tta ttg aga gct ggt tgg aat gag ttg atg att gca gca ttt	672
Val Leu Leu Leu Arg Ala Gly Trp Asn Glu Leu Met Ile Ala Ala Phe	
210 215 220	
tcc cat aga tca atc agt gta aaa gat ggt ata gtc tta gct act gga	720
Ser His Arg Ser Ile Ser Val Lys Asp Gly Ile Val Leu Ala Thr Gly	
225 230 235 240	
ctt act gtt gac aga gat tca gct cac caa gct ggt gtt gaa gct ata	768
Leu Thr Val Asp Arg Asp Ser Ala His Gln Ala Gly Val Glu Ala Ile	
245 250 255	
ttt gat cgt gta ctc act gaa ctc gtt gct aaa atg aga gat atg ggt	816
Phe Asp Arg Val Leu Thr Glu Leu Val Ala Lys Met Arg Asp Met Gly	
260 265 270	
atg gat aga aca gag ctt ggc tgt ttg cgt act att att ctt ttt aat	864
Met Asp Arg Thr Glu Leu Gly Cys Leu Arg Thr Ile Ile Leu Phe Asn	
275 280 285	
cca ggt tca aaa ggt ttg cag tct gtg aat gaa gtg caa gta ctg cgt	912

Pro Gly Ser Lys Gly Leu Gln Ser Val Asn Glu Val Gln Val Leu Arg
 290 295 300

gat aag gtt tat gtt gcg tta gaa gaa tat tgt cgt aca aca cat cca 960
 Asp Lys Val Tyr Val Ala Leu Glu Glu Tyr Cys Arg Thr Thr His Pro
 305 310 315 320

gaa gaa cct gga cga ttt gct aaa cta ctt ctt cgg ctt cct tca tta 1008
 Glu Glu Pro Gly Arg Phe Ala Lys Leu Leu Leu Arg Leu Pro Ser Leu
 325 330 335

cgt tca att gga tta aaa tgt ctg gaa cat tta ttc ttt tat aaa ctt 1056
 Arg Ser Ile Gly Leu Lys Cys Leu Glu His Leu Phe Phe Tyr Lys Leu
 340 345 350

att ggc gat tcc cca att gat aca ttt tta atg gaa gtt ctc gaa tca 1104
 Ile Gly Asp Ser Pro Ile Asp Thr Phe Leu Met Glu Val Leu Glu Ser
 355 360 365

tct tca cat gac gtt caa gta gct aca 1131
 Ser Ser His Asp Val Gln Val Ala Thr
 370 375

<210> 12

<211> 377

<212> PRT

<213> Myzus persicae

<400> 12

Met Tyr Ser Asn Ser Tyr Thr Met Tyr Ser Ser Asp Arg Leu Tyr Ser
 1 5 10 15

Val Asp Arg Asn Ser Met Met Asn Asn Ser Cys Asn Val Gln Asp Ser
 20 25 30

Pro Asn Tyr Pro Pro Asn His Pro Leu Ser Gly Ser Lys His Leu Cys
 35 40 45

Ser Ile Cys Gly Asp Arg Ala Ser Gly Lys His Tyr Gly Val Tyr Ser
 50 55 60

Cys Glu Gly Cys Lys Gly Phe Phe Lys Arg Thr Val Arg Lys Asn Leu
 65 70 75 80

Ser Tyr Ala Cys Arg Glu Glu Asn Lys Cys Ile Ile Asp Lys Arg Gln
 85 90 95

Arg Asn Arg Cys Gln Tyr Cys Arg Tyr Gln Lys Cys Leu Thr Met Gly
 100 105 110

Met Lys Arg Glu Ala Val Gln Glu Glu Arg Gln Arg Thr Lys Glu Arg
 115 120 125
 Asp His Asn Asn Ile Glu Val Glu Pro Thr Ser Ser Ser Asn Thr Asp
 130 135 140
 Met Pro Val Glu Leu Ile Leu Arg Ala Glu Asn Lys Ala Asp Ala Ile
 145 150 155 160
 Lys Thr Glu Gln Gln Tyr Ile Glu Gln Arg His Pro Gln His Thr Val
 165 170 175
 Gly Ala Ile Cys Gln Ala Thr Asp Lys Gln Leu Ile Gln Leu Val Glu
 180 185 190
 Trp Ala Lys His Ile Pro His Phe Lys Asn Leu Pro Leu Gly Asp Gln
 195 200 205
 Val Leu Leu Leu Arg Ala Gly Trp Asn Glu Leu Met Ile Ala Ala Phe
 210 215 220
 Ser His Arg Ser Ile Ser Val Lys Asp Gly Ile Val Leu Ala Thr Gly
 225 230 235 240
 Leu Thr Val Asp Arg Asp Ser Ala His Gln Ala Gly Val Glu Ala Ile
 245 250 255
 Phe Asp Arg Val Leu Thr Glu Leu Val Ala Lys Met Arg Asp Met Gly
 260 265 270
 Met Asp Arg Thr Glu Leu Gly Cys Leu Arg Thr Ile Ile Leu Phe Asn
 275 280 285
 Pro Gly Ser Lys Gly Leu Gln Ser Val Asn Glu Val Gln Val Leu Arg
 290 295 300
 Asp Lys Val Tyr Val Ala Leu Glu Glu Tyr Cys Arg Thr Thr His Pro
 305 310 315 320
 Glu Glu Pro Gly Arg Phe Ala Lys Leu Leu Leu Arg Leu Pro Ser Leu
 325 330 335
 Arg Ser Ile Gly Leu Lys Cys Leu Glu His Leu Phe Phe Tyr Lys Leu
 340 345 350
 Ile Gly Asp Ser Pro Ile Asp Thr Phe Leu Met Glu Val Leu Glu Ser
 355 360 365
 Ser Ser His Asp Val Gln Val Ala Thr
 370 375

<210> 13
<211> 150
<212> DNA
<213> Lucilia cuprina

<220>
<221> CDS
<222> (9)..(134)

<400> 13
aattctgc gaa gga tgc aag gga ttc ttc aaa cgt acc gta cgc aag gac 50
Glu Gly Cys Lys Gly Phe Phe Lys Arg Thr Val Arg Lys Asp
1 5 10

ttg aca tat gct tgt cgt gag gac aga aat tgc att ata gat aaa cga 98
Leu Thr Tyr Ala Cys Arg Glu Asp Arg Asn Cys Ile Ile Asp Lys Arg
15 20 25 30

caa aga aat cgt tgc cag tat tgt cgc tac caa aag tgatcgatac cgtcga 150
Gln Arg Asn Arg Cys Gln Tyr Cys Arg Tyr Gln Lys
35 40

<210> 14
<211> 42
<212> PRT
<213> Lucilia cuprina

<400> 14
Glu Gly Cys Lys Gly Phe Phe Lys Arg Thr Val Arg Lys Asp Leu Thr
1 5 10 15

Tyr Ala Cys Arg Glu Asp Arg Asn Cys Ile Ile Asp Lys Arg Gln Arg
20 25 30

Asn Arg Cys Gln Tyr Cys Arg Tyr Gln Lys
35 40

<210> 15
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:oligonucleotide
useful as primer.

<220>
<221> misc_feature
<222> (1)..(32)

<223> Nucleotides designated as "n" residues can be A,
G, C or T residues.

<400> 15

cggaattccg cctcnggnta ycaytayaay gc

32

<210> 16

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Oligonucleotide
useful as primer.

<400> 16

cgcggatccr cactcctgac actttcgyct ca

32

<210> 17

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Oligonucleotide
useful as primer.

<400> 17

gcctcggggt atcactataa cgc

23

<210> 18

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Oligonucleotide
useful as primer.

<400> 18

gcactcctga cactttcgtc tca

23

<210> 19

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Oligonucleotide
useful as primer.

<400> 19

tcgtccggtt accattacaa cgc

23

<210> 20

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<221> misc_feature

<222> (1)..(24)

<223> Nucleotides designated as "n" residues can be A,
G, C or T residues.

<400> 20

tagacctttg gcraaytcna caat

24